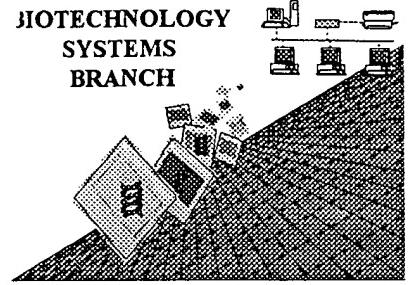


Haimud

RAW SEQUENCE LISTING

ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/037,657

Art Unit / Team No.: 1646

Date Processed by STIC: 6/30/89

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/037,657DATE: 06/30/1999
TIME: 14:43:20

Input Set: I037657.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

Reel
P. S. 1 Job

1 <110> APPLICANT: Hilton, Douglas J.
2 Nicola, Nicos A.
3 Farley, Alison
4 Wilson, Tracy
5 Zhang, Jian-Guo
6 Alexander, Warren
7 Rakar, Steven
8 Fabri, Louis
9 Kojima, Tetsuo
10 Maeda, Masatsugu
11 Kikuchi, Yasufumi
12 Nash, Andrew
13 <120> TITLE OF INVENTION: A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES
14 ENCODING SAME
15 <130> FILE REFERENCE: DAVIES COLLISON CAVE (CIP)
16 <140> CURRENT APPLICATION NUMBER: US/09/037,657
17 <141> CURRENT FILING DATE: 1998-03-10
18 <150> EARLIER APPLICATION NUMBER: 08/928,720
19 <151> EARLIER FILING DATE: 1997-09-11
20 <160> NUMBER OF SEQ ID NOS: 54
21 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO 1
23 <211> LENGTH: 5
24 <212> TYPE: PRT
25 <213> ORGANISM: Unknown *see item 12 or Env summary sheet*
26 <220> FEATURE:
27 <221> NAME/KEY: UNSURE
28 <222> LOCATION: (3)
29 <223> OTHER INFORMATION: Unsure at position 3
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32 1 5
33 <210> SEQ ID NO 2
34 <211> LENGTH: 24
35 <212> TYPE: DNA
36 <213> ORGANISM: Artificial Sequence
37 <220> FEATURE:
38 <223> OTHER INFORMATION: Description of Artificial Sequence: M116 probe
39 <400> SEQUENCE: 2
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41 <210> SEQ ID NO 3
42 <211> LENGTH: 24
43 <212> TYPE: DNA
44 <213> ORGANISM: Artificial Sequence

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45 <220> FEATURE:
46 <223> OTHER INFORMATION: Description of Artificial Sequence:M108 probe
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49 <210> SEQ ID NO 4
50 <211> LENGTH: 24
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
53 <220> FEATURE:
54 <223> OTHER INFORMATION: Description of Artificial Sequence:M159 probe
55 <400> SEQUENCE: 4
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57 <210> SEQ ID NO 5
58 <211> LENGTH: 24
59 <212> TYPE: DNA
60 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
62 <223> OTHER INFORMATION: Description of Artificial Sequence:M242 probe
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65 <210> SEQ ID NO 6
66 <211> LENGTH: 22
67 <212> TYPE: DNA
68 <213> ORGANISM: Artificial Sequence
69 <220> FEATURE:
70 <223> OTHER INFORMATION: Description of Artificial Sequence:M112 probe
71 <400> SEQUENCE: 6
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73 <210> SEQ ID NO 7
74 <211> LENGTH: 15
75 <212> TYPE: DNA
76 <213> ORGANISM: Unknown
77 <220> FEATURE:
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79 <220> FEATURE:
80 <221> NAME/KEY: unsure
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82 <223> OTHER INFORMATION: Unsure at position 1
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89 <222> LOCATION: (10)
90 <223> OTHER INFORMATION: Unsure at position 10
91 <400> SEQUENCE: 7
92 rctccartcr ctcca 15
93 <210> SEQ ID NO 8
94 <211> LENGTH: 15

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RAW SEQUENCE LISTING
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95 <212> TYPE: DNA
96 <213> ORGANISM: Unknown
97 <220> FEATURE:
98 <223> OTHER INFORMATION: Description of Unknown Organism:Unsure
99 <220> FEATURE:
100 <221> NAME/KEY: unsure
101 <222> LOCATION: (1)
102 <223> OTHER INFORMATION: Unsure at position 1
103 <220> FEATURE:
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105 <222> LOCATION: (7)
106 <223> OTHER INFORMATION: Unsure at position 7
107 <220> FEATURE:
108 <221> NAME/KEY: unsure
109 <222> LOCATION: (10)
110 <223> OTHER INFORMATION: Unsure at position 10
111 <400> SEQUENCE: 8
112 rctccaytcr ctcca 15
113 <210> SEQ ID NO 9
114 <211> LENGTH: 21
115 <212> TYPE: DNA
116 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Description of Artificial Sequence:1944 probe
119 <400> SEQUENCE: 9
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121 <210> SEQ ID NO 10
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123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: Description of Artificial Sequence:2106 probe
127 <400> SEQUENCE: 10
128 ggaggtgtta aggaggcg 18
129 <210> SEQ ID NO 11
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131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: Description of Artificial Sequence:2120 probe
135 <400> SEQUENCE: 11
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138 <211> LENGTH: 1629
139 <212> TYPE: DNA
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141 <220> FEATURE:
142 <221> NAME/KEY: CDS
143 <222> LOCATION: (124)..(1362)
144 <220> FEATURE:

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RAW SEQUENCE LISTING
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145 <223> OTHER INFORMATION: Description of Unknown Organism:Murine NR6.1
 146 <400> SEQUENCE: 12
 147 ggcacgagct tcgctgtccg cgcccagtga cgcgctgtcg gaccggagcc ccaatctgca 60
 148 ccccgccagac tcgccccccgc cccataccgg cgttgcagtc accgcccgtt gcgcgccacc 120
 149 ccc atg ccc gcg ggt cgc ccg ggc ccc gtc gcc caa tcc gcg cgg cgg 168
 Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg
 150 1 5 10 15
 151 ccg ccg cgg ccg ctg tcc tcg ctg tgg tcg cct ctg ttg ctc tgt gtc 216
 152 Pro Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Cys Val
 153 20 25 30
 154 ctc ggg gtg cct cgg ggc gga tcg gga gcc cac aca gct gta atc agc 264
 155 Leu Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser
 156 35 40 45
 157 ccc cag gac ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc 312
 158 Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys
 159 50 55 60
 160 tct ata cat gga gac aca cct ggg gcc acc gct gag ggg ctc tac tgg 360
 161 Ser Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp
 162 65 70 75
 163 acc ctc aat ggt cgc cgc ctg ccc tct gag ctg tcc cgc ctc ctt aac 408
 164 Thr Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn
 165 80 85 90 95
 166 acc tcc acc ctg gcc ctg gcc ctg gct aac ctt aat ggg tcc agg cag 456
 167 Thr Ser Thr Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
 168 100 105 110
 169 cag tca gga gac aat ctg gtg tgt cac gcc cga gac ggc agc att ctg 504
 170 Gln Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
 171 115 120 125
 172 gct ggc tcc tgc ctc tat gtt ggc ttg ccc cct gag aag ccc ttt aac 552
 173 Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn
 174 130 135 140
 175 atc agc tgc tgg tcc cgg aac atg aag gat ctc acg tgc cgc tgg aca 600
 176 Ile Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
 177 145 150 155
 178 ccg ggt gca cac ggg gag aca ttc tta cat acc aac tac tcc ctc aag 648
 179 Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys
 180 160 165 170 175
 181 tac aag ctg agg tgg tac ggt cag gat aac aca tgt gag gag tac cac 696
 182 Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His
 183 180 185 190
 184 act gtg ggc cct cac tca tgc cat atc ccc aag gac ctg gcc ctc ttc 744
 185 Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe
 186 195 200 205
 187 act ccc tat gag atc tgg gtg gaa gcc acc aat cgc cta ggc tca gca 792
 188 Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala
 189 210 215 220
 190 aga tct gat gtc ctc aca ctg gat gtc ctg gac gtg gtg acc acg gac 840
 191 Arg Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp
 192 225 230 235
 193 ccc cca ccc gac gtg cac gtg agc cgc gtt ggg ggc ctg gag gac cag 888
 194

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195 Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln
 196 240 245 250 255
 197 ctg agt gtg cgc tgg gtc tca cca cca gct ctc aag gat ttc ctc ttc 936
 198 Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe
 199 260 265 270
 200 caa gcc aag tac cag atc cgc tac cgc gtg gag gac agc gtg gac tgg 984
 201 Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp
 202 275 280 285
 203 aag gtg gtg gat gac gtc agc aac cag acc tcc tgc cgt ctc gcg ggc 1032
 204 Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly
 205 290 295 300
 206 ctg aag ccc ggc acc gtt tac ttc gtc caa gtg cgt tgt aac cca ttc 1080
 207 Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe
 208 305 310 315
 209 ggg atc tat ggg tcg aaa aag gcg gga atc tgg agc gag tgg agc cac 1128
 210 Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His
 211 320 325 330 335
 212 ccc acc gct gcc tcc acc cct cga agt gag cgc ccg ggc ccg ggc 1176
 213 Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly
 214 340 345 350
 215 ggg gtg tgc gag ccg cgg ggc gag ccc agc tcg ggc ccg gtg cgg 1224
 216 Gly Val Cys Glu Pro Arg Gly Glu Pro Ser Ser Gly Pro Val Arg
 217 355 360 365
 218 cgc gag ctc aag cag ttc ctc ggc tgg ctc aag aag cac gca tac tgc 1272
 219 Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys
 220 370 375 380
 221 tcg aac ctt agt ttc cgc ctg tac gac cag tgg cgt gct tgg atg cag 1320
 222 Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln
 223 385 390 395
 224 aag tca cac aag acc cga aac cag gtc ctg ccg gct aaa ctc 1362
 225 Lys Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu
 226 400 405 410
 227 taaggatagg ccatcctcct gctgggtcag acctggaggc tcacctgaat tggagcccct 1422
 228 ctgtaccatc tggcaacaa agaaacctac cagaggctgg ggcacaatga gctcccacaa 1482
 229 ccacagctt ggtcccacatg atggcacac ttggatatac cccagtgtgg gtaaggttgg 1542
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 231 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1629
 232 <210> SEQ ID NO 13
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 234 <212> TYPE: PRT
 235 <213> ORGANISM: Unknown
 236 <220> FEATURE:
 237 <223> OTHER INFORMATION: Description of Unknown Organism: Murine NR6.1
 238 <400> SEQUENCE: 13
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 239 1 5 10 15
 Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu
 240 20 25 30
 Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
 241 35 40 45

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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VERIFICATION SUMMARY
PATENT APPLICATION US/09/037,657

DATE: 06/30/1999
TIME: 14:43:20

Input Set: I037657.RAW

Line ? Error/Warning

Original Text

31 W "N" or "Xaa" used: Feature required
1030 W "N" or "Xaa" used: Feature required
1034 W "N" or "Xaa" used: Feature required
1036 W "N" or "Xaa" used: Feature required

Trp Ser Xaa Trp Ser
Leu Arg Leu Val Arg Ser Glu Xaa His Met X
Leu Xaa Asp Leu Gly Gly Ser His Gln Ser P
Xaa Cys Pro His Thr Gly Cys Pro Gly Arg

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/039,657

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: -
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.